

-continued

<220> FEATURE:

<223> OTHER INFORMATION: primer

<400> SEQUENCE: 25

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1. A method for selecting a plant from a plant population by genotyping, the method comprising:

- a) isolating genomic DNA of individual plants or individual plant seeds separately, to provide separate DNA samples;
- b) amplifying a desired target sequence of said DNA samples with target-specific primers, wherein each target-specific primer comprises a target-specific hybridization sequence and an adapter sequence, wherein at least one of the primers contains a barcode sequence, whereby the resulting amplification products (amplicons) comprise the target sequence, the adapter sequences and the barcode sequence;
- c) pooling the amplicons of step (b) to prepare an amplicon library;
- d) sequencing said amplified target sequence by using a next generation sequencing (NGS) technique; and
- e) comparing the target-sequence with a known sequence of said target-sequence, wherein the target-sequence can be allocated to an individual plant by the barcode sequence.

2. The method according to claim 1, wherein several different target sequences are amplified simultaneously.

3. The method according to claim 1, wherein the method comprises:

- a) isolating genomic DNA of individual plants or individual plant seeds separately, to provide separate DNA samples;
- b) amplifying in parallel a plurality of different desired target sequences of said DNA samples with target-specific primers either separately or in a multiplex PCR reaction, wherein each target-specific primer comprises a target-specific hybridization sequence and an adapter sequence, wherein at least one of the primers contains a barcode sequence, whereby the resulting amplification products (amplicons) comprise the target sequence, the adapter sequences and the barcode sequence;
- c) pooling the amplicons of step (b) to prepare an amplicon library;
- d) sequencing said amplified target sequences by using a next generation sequencing (NGS) technique; and
- e) comparing the target-sequences with known sequences of said target-sequences, wherein the target-sequences can be allocated to an individual plant by the barcode sequences.

4. The method according to claim 1, wherein said target sequence is selected from the group consisting of a polynucleotide, a nucleic acid pattern and a genomic region, optionally the target sequence is a Quantitative Trait Loci (QTL).

5. The method according to claim 1, wherein a plurality of individual plants are genotyped in parallel, and wherein the genomic DNA of a plurality of individual plants are isolated and amplified without pooling the genomic DNA before amplifying.

6. The method according to claim 1, wherein the target sequence is a chromosomal segment that comprises a portion of a natural or artificial genetic rearrangement, wherein the genetic rearrangement is optionally selected from the group consisting of an inversion, an insertion, a deletion, and a translocation.

7. The method according to claim 1, wherein the target sequence comprises a variation, optionally a Single Nucleotide Polymorphism (SNP).

8. The method according to claim 1, wherein the target sequence comprises a mutation, or a target portion or a flanking portion.

9. The method according to claim 8, wherein the target-specific hybridization sequence in the primer is complementary to a flanking portion.

10. The method according to claim 8, wherein the target-specific hybridization sequence is complementary to parts of the target portion.

11. The method according to claim 1, wherein the barcode sequence has a length of 4 or more nucleotides, optionally between 4 and 8 nucleotides.

12. The method according to claim 1, wherein the barcode sequence is located between the target-specific hybridization sequence and the adapter sequence.

13. The method according to claim 1, wherein the amplicon has a length between 100 and 1000 bp, optionally between 200 and 800 bp, between 200 and 600 bp, or between 200 and 400 bp.

14. The method according to claim 1, wherein the next generation sequencing method applied is selected from the group of sequencing by synthesis, pyrosequencing, ion semiconductor technology sequencing, and single molecule real-time sequencing.

15. The method according to claim 1, for screening a plant or a plant population for multiple characteristics.

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